

FIGURE 1A

1 CCGCAGCAAAGGAACGTGCGAACGCGTGACGCCGCCGACTGGCTCGCGCTCTCCCGTGC
61 CCCGCGTGCTCCTCCGCCCGCTCATGGCCCGGGCCGCCGCGGACGAGCGGCGCTGAGGCGGG
121 CCGCGTGGAGACGTGAGGCGGCCGCCGCTGGCCCTCACAGTCGGCGTTTCGCCCGCCTGCC
181 GCGGTGCCCCGCGCACGCGCTGCCGCCATCGCCTTCGCGCCTGGCTGGCGGGGGCGCTGTCC
241 TCCCAGGCCGTCCGCGCGCTCCTTGAGCTCGGCGGAGCGCGGCAGCCAGGGCCGGCGG
301 AGGCGCGAGGAGCCGGGCGCCACCGCCGCCGCCGCCGCCGCCGGGGGCCATGACC
361 GTGGAGCAGAACGTGCTGCAGCAGAGCGGCGCAGAAGCACCAGCAGACGTTTTTGAAT
421 CAACTGAGAGAAATTACGGGGATTAATGACACCCAGATACTACAGCAAGCCTTGAAGGAT
481 AGTAATGGAAC'TTGGAATTAGCAGTGCTTTTCTTACTGCGAAGAATGCTAAGACCCCT
541 CAGCAGGAGGAGACAAC'TTACTACCAACAGCACTTCTTGGCAATGATAGATACATCAGT
601 GTGGGAAGCCAAGCAGATACAAATGTGATTGATCTCAGTGGAGATGATAAAGATGATCTT
661 CAGAGAACAATTGCCTTGAGTTTGCCGAATCAAACAGGGCATTTCAGGGAGACTGGAATA
721 ACTGATGAGGAACAAGCCATTAGCAGAGTTCTTGAAGCCAGTATAGCAGAGAATAAAGCA
781 TGTTTGAAGAGGACACCTACAGAAGTTTGAGGGATTCTCGAAACCCCTTATGATAGAAAA
841 AGACAGGACAAAGCTCCCGTTGGGCTAAAGAATGTTGGCAATACTTGTGGTTTGTAGTCT
901 GTTATTTCAGTCATTATTTAATCTTTTGAATTTAGAAGATTAGTTCTGAATTACAAGCCT
961 CCATCAAATGCTCAAGATTTACCCCGAAACCAAAAGGAACATCGGAATTTGCCTTTTATG
1021 CGTGAGCTGAGGTATCTATTTGCACTTCTTGTGGTACCAAAAGGAAGTATGTTGATCCA
1081 TCAAGAGCAGTTGAAATCTTAAGGATGCTTTCAAATCAAATGACTCACAGCAGCAAGAT
1141 GTGAGTGAGTTTACACACAAATTTATGAGTTGGTTAGAAGATGCCTTCAAATGAAAGCT
1201 GAAGAGGAGACGGATGAAGAGAAGCCAAAGAACCCCATGGTAGAGTTGTTCTATGGCAGA
1261 TTCCTGGCTGTGGGAGTACTTGAAGGTAAAAAATTTGAAAACACTGAAATGTTTGGTCAG
1321 TACCCACTTCAGGTCAATGGGTCAAAGATCTGCATGAGTGCCTAGAAGCTGCAATGATT
1381 GAAGGAGAAATTGAGTCTTTACATTTCAGAGAATTCAGGAAAATCAGGCCAAGAGCATTGG
1441 TTTACTGGATTACCACCTGTGTTAACATTTGANTTGTCAAGATTTGAATTTAATCAGGCA
1501 TTGGGAAGACCAGAAAAAATTCACAACAAATTAGAATTTCCCCAAGTTTATATTTGGAC
1561 AGATACATGCACAGAAACAGAGAAATAACAAGAATTAAGAGGGAAGAGATCAAGAGACTG
1621 AAAGATTACCTCACGGTATTACAACAAAGGCTAGAAAGATATTTAAGCTATGGTTCCGGT
1681 CCCAAACGATTCCCTTGGTAGATGTTCTTCAGTATGCATTGGAATTTGCCTCAAGTAAA
1741 CCTGTTTGCACCTTCTCCTGTTGACGATATTGACGCTAGTTCCCCACCTAGTGGTTCCATA
1801 CCATCACAGACATTACCAAGCACAAACAGAAACAACAGGGAGCCCTATCTTCAGAACTGCCA
1861 AGCACATCACCTTCATCAGTTGCTGCCATTTTCATCGAGATCAGTAATACACAAACCATTT
1921 ACTCAGTCCCGGATACCTCCAGATTTGCCCATGCATCCGGCACCAAGGCACATAACGGAG
1981 GAAGAACTTTCTGTGCTGGAAAGTTGTTTACATCGCTGGAGGACAGAAATAGAAAATGAC
2041 ACCAAGATTTGCAGGAAAGCATATCCGAATCCATCGAACAATTGAATTAATGTACTCT
2101 GACAAATCTATGATACAAAGTTCTTATCGATTACATGCCGTTTTAGTTTACGAAGGCCAA
2161 GCTAATGCTGGGCACTACTGGGCATATATTTTTGATCATCGTGAAAGCAGATGGATGAAG
2221 TACAATGATATTGCTGTGACAAAATCATCATGGGAAGAGCTAGTGAGGGACTCTTTTGGT
2281 GGTTATAGAAATGCCAGTGCATACTGTTTAAATGTACATAAATGATAAGGCACAGTTCCTA
2341 ATACAAGAGGAGTTTAAATAAGAACTGGGCAGCCCCCTTGTGGTATAGAAACATTACCA
2401 CCGGATTTGAGAGATTTTGTGAGGAAGACAACCAACGATTTGAAAAAGAACTAGAAGAA
2461 TGGGATGCACAACTTGCCCGAAAGCTTTGCAGGAAAAGCTTTTAGCGTCTCAGAAATTG
2521 AGAGATCAGAGACTTCTGTGACAACAGCACAGCAGCAGGAGACCCAGAATATCTAGAG
2581 CAGCCATCAAGAAGTGATTTCTCAAAGCACTTGAAAGAAGAACTATTCAAATAATTACC
2641 AAGGCATCATATGAGCATGAAGATAAAAGTCTTGAAACAGTTTTTGCAGTCGGCAATTAAG
2701 TTGGAATATGCAAGGTTGGTTAAGTTGGCCCAAGAAGACACCCACCAGAAACCGATTAT
2761 CGTTTACATCATGTAGTGGTCTACTTTATCCAGAACCAGGCACCAAGAAAATTATTGAG
2821 AAAACATTACTAGAACAATTTGGAGATAGAAAATTTGAGTTTTGATGAAAGGTGTCACAAC
2881 ATAATGAAAGTTGCTCAAGCCAAACTGGAATGATAAAACCTGAAGAAGTAACTTGGAG
2941 GAATATGAGGAGTGGCATCAGGATTATAGGAAATTCAGGAAAACAACATATGTATCTCATA
3001 ATTGGGCTAGAAAAATTTTCAAAGAGAAAGTTATATAGATTCTTGCTGTTTCTCATCTGT
3061 GCTTATCAGAATAACAAAGAACTCTTGTCTAAAGGCTTATACAGAGGACATGATGAAGAA
3121 TTGATATCACATTATAGAAGAGAATGTTTGCTAAAATTAATGAGCAAGCCGCAGAATC
3181 TTCGAATCTGGAGAGGATCGAGAAGTAACAATGGTTTGATTATCATGAATGAGTTTATT
3241 GTCCCATTTTTGCCATTATTACTGGTGGATGAAATGGAAGAAAAGGATATACTAGCTGTA
3301 GAAGATATGAGAAATCGATGGTGTTCCTACCTTGGTCAAGAAATGGAACCACACCTCCAA
3361 GAAAAGCTGACAGATTTTTTGCCAAAACCTGCTTGATTGTTCTATGGAGATTAAAAGTTTC

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3421 CATGAGCCACCGAAGTTACCTTCATATTCCACGCATGAACTCTGTGAGCGATTGCCCCGA
3481 ATCATGTTGTCCCTCAGTCGAACTCCTGCTGATGGAAGATTAAACTGCACACTTTCCTGA
3541 ACACACTGTATAAACTCTTTTGTAGTTCTTAACCTTGCCTTCCTGTCACAGGGTTTGCTT
3601 GTTGCTGCTATAGTTTTTAACTTTTTTTTATTTAATAACTGCAAAAGACAAAATGACTA
3661 TACAGACTTTAGTCAGACTGCAGACAATAAAGCTGAAAATCGCATGGCGCTCAGACATTT
3721 TAACCGGAACTGATGTATAATCACAAATCTAATTGATTTTATTATGGCAAACTATGCTT
3781 TTGCCACCTTCCTGTTGCAGTATTACTTTGCTTTTATCTTTTCTTCTCAACAGCTTTCC
3841 ATTCACTCTGGATCCTTCCATGACTACAGCCATTTAAGTGTTTCAGCACTGTGTACGATAC
3901 ATAATATTTGGTAGCTTGTAATGAAATAAAGAATAAAGTTTTATTATGGCTAC

FIGURE 1B

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FIGURE 2

1 MTVEQNVLQQSAAQKHQQTFNLNQLREITGINDTQILQQALKDSNGNLELAVAFITAKNAK
61 TPQQEETTYQTALPGNDRIYISVGSQADTNVIDLTGDDKDDLQRTIALSLAESNRAFRET
121 GITDEEQAISRVLEASIAENKACLKRTPTFVWRDSRNPYDRKRQDKAPVGLKNVGNLCWF
181 SAVIQSLFNLLEFRRLVLNYPKPPSNAQDLPRNQKEHRNLPFMRELRYLFALLVGTGRKYV
241 DPSRAVEILKDAFKSNSDQQQDVSEFTHKLLDWLEDAFQMKAEETDEEKPKNPMVELFY
301 GRFLAVGVLEGKKFENTEMFGQYPLQVNGFKDLHECLEAAMIEGEIESLHSENSGKSGQE
361 HWFTGLPPVLTFXLSRFEFNQALGRPEKIHNNKLEFPQVLYLDRYMHRNREITRIKREEIK
421 RLKDYLTVLQQRLERYLSYSGSGPKRFPLVDVLQYALEFASSKPVCTSPVDDIDASSPPSG
481 SIPSQTLPTSTTEQQGALSSELPSTSPSSVAAISSRSVIHKPFTQSRIPDLPMHPAPRHI
541 TEEELSVLESCLRWRTEIENDTRDLQESISRIHRTIELMYSKSMIQVPYRLHAVLVHE
601 GQANAGHYWAYIFDHRESRWKMYNDIAVTKSSWEELVRDSFGGYRNASAYCLMYINDKAQ
661 FLIQEEFNKETGQPLVGIEITLPPDLRDFVEEDNQRFKELEEWDAQLAQKALQEKLLASQ
721 KLRESESVTTAAQAAGDPEYLEQPSRSDFSKHLKEETIQIITKASHEHEDKSPETVLQSA
781 IKLEYARLVKLAQEDTPPETDYRLHHVVVYFIQNQAPKKIIEKTLLEQFGDRNLSFDERC
841 HNIMKVAQAKLEMIKPEEVNLEEYEEWHQDYRKFRETTMYLIIGLENFQRESYIDSLFL
901 ICAYQNNKELLSKGLYRGHDEELISHYRRECLLKLNEQAELFESGEDREVNNGLIIMNE
961 FIVPFLPLLLVDEMEEKDILAVEDMRNRWCSYLGQEMEPHLQEKLTDFLPKLLDCSMEIK
1021 SFHEPPKLPSYSTHELCECFARIMLSLRTPADGR

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FIGURE 3A

1 CGGCAGCAAAGGAACGTGCGAACGCGTGACGCCGCCGACTGGCTCGCGCTCTCCCGTGC
61 CCCGGCGTCTCCGCCCGCTCATGGCCCGGGCCGCCGCGGACGAGCGGCGCTGAGGCGGG
121 CCGCGTGAGACGTGAGGCGGCCCGCTGGCCCTCACAGTCGGCGTTTCGCCGCTGCC
181 GCGGTGCCCCGCGCACGCTGCCGCCATCGCCTTCGCGCCTGGCTGGCGGGGGCGCTGTCC
241 TCCCAGGCCGTCCGCGCCGCTCCCTGGAGCTCGGCGGAGCGCGGCAGCCAGGGCCGCGG
301 AGGCGCGAGGAGCCGGGCGCCACCGCCGCCGCCGCCGCCGCCGCCGGGGGCCATGACC
361 GTGGAGCAGAACGTGCTGTCAGCAGAGCGCGGCGCAGAAGCACCAGCAGACGTTTTTGAAT
421 CAACTGAGAGAAATTACGGGGATTAATGACACCCAGATACTACAGCAAGCCTTGAAGGAT
481 AGTAATGGAAACTTGAATTAGCAGTGGCTTTCCTTACTGCGAAGAATGCTAAGACCCCT
541 CAGCAGGAGGAGACAACCTTACTACCAAACAGCACTTCTTGCAATGATAGATACATCAGT
601 GTGGGAAGCCAAGCAGATACAAATGTGATTGATCTCACTGGAGATGATAAAGATGATCTT
661 CAGAGAACAATTGCCTTGAGTTTGGCCGAATCAAACAGGCGATTTCAGGGAGACTGGAATA
721 ACTGATGAGGAACAAGCCATTAGCAGAGTTCTTGAAGCCAGTATAGCAGAGAATAAAGCA
781 TGTTTGAAGAGGACACCTACAGAAGTTTGGAGGGATTCTCGAAACCCCTTATGATAGAAAA
841 AGACAGGACAAAGCTCCCGTTGGGCTAAAGAATGTTGGCAATACTTGTTGGTTTAGTGCT
901 GTTATTCAGTCATTATTTAATCTTTTGAATTTAGAAGATTAGTTCTGAATTACAAGCCT
961 CCATCAAATGCTCAAGATTTACCCCGAAACCAAAGGAACATCGGAATTTGCCTTTTATG
1021 CGTGAGCTGAGGTATCTATTTGCACCTTCTTGTGGTACCAAAGGAAGTATGTTGATCCA
1081 TCAAGAGCAGTTGAAATTCTTAAGGATGCTTTCAAATCAAATGACTCACAGCAGCAAGAT
1141 GTGAGTGAGTTTACACACAAATTATTAGATTGGTTAGAAGATGCCTTCCAAATGAAAGCT
1201 GAAGAGGAGACGGATGAAGAGAAGCCAAAGAACCCCATGGTAGAGTTGTTCTATGGCAGA
1261 TTCTTGGCTGTGGGAGTACTTGAAGGTAAAAATTTGAAAACACTGAAATGTTTGGTCAG
1321 TACCCACTTCAGGTCAATGGGTTCAAAGATCTGCATGAGTGCCTAGAAGCTGCAATGATT
1381 GAAGGAGAAATTGAGTCTTTACATTACAGAGAATTCAGGAAAATCAGGCCAAGAGCATTGG
1441 TTTACTGGATTACCACCTGTGTTAACATTTGANTTGTCAAGATTTGAATTTAATCAGGCA
1501 TTGGGAAGACCAGAAAAAATTCACAACAATTAGAATTTCCCAAGTTTATATTTGGAC
1561 AGATACATGCACAGAAACAGAGAAATAACAAGAATTAAAGAGGAAGAGATCAAGAGACTG
1621 AAAGATTACCTCACGGTATTACAACAAGGCTAGAAAGATATTTAAGCTATGGTTCCGGT
1681 CCCAAACGATTCCCCTTGGTAGATGTTCTTCAGTATGCATTGGAATTTGCCTCAAGTAAA
1741 CCTGTTTGCACTTCTCCTGTTGACGATATTGACGCTAGTTCCCCACCTAGTGGTTCCATA
1801 CCATCACAGACATTACCAAGCACAAACAGAACACAGGGAGCCCTATCTTCAGAACTGCCA
1861 AGCACATCACCTTCATCAGTTGCTGCCATTTTCATCGAGATCAGTAATACACAAACCATTT
1921 ACTCAGTCCCGGATACCTCCAGATTGCCCCATGCATCCGGCACCAAGGCACATAACGGAG
1981 GAAGAATTTCTGTGTGCGAAAGTTGTTTACATCGCTGGAGGACAGAAATAGAAAATGAC
2041 ACCAGAGATTTGCGAGGAAAGCATATCCGAATCCATCGAACAATTGAATTAATGTACTCT
2101 GACAAATCTATGATACAAGTTCCTTATCGATTACATGCCGTTTTAGTTTCACGAAGGCCAA
2161 GCTAATGCTGGGCACTACTGGGCATATATTTTTGATCATCGTGAAAGCAGATGGATGAAG
2221 TACAATGATATTGCTGTGACAAAATCATCATGGGAAGAGCTAGTGAGGGACTCTTTTGGT
2281 GGTATAGAAATGCCAGTGCATACTGTTTAATGTACATAAATGATAAGGCACAGTTCCTA
2341 ATACAAGAGGAGTTTAATAAAGAACTGGGCAGCCCCCTGTTGGTATAGAAACATTACCA
2401 CCGGATTTGAGAGATTTTGTGAGGAAGACAACCAACGATTTGAAAAAGAACTAGAAGAA
2461 TGGGATGCACAACCTTGCCAGAAAGCTTTGCGAGGAAAAGCTTTAGCGTCTCAGAAATTG
2521 AGAGAGTCAGAGACTTCTGTGACAACAGCACAAAGCAGCAGGAGACCCAGAAATATCTAGAG
2581 CAGCCATCAAGAAGTGATTTCTCAAAGCACTTGAAAGAAGAACTATTCAAATAATTACC
2641 AAGGCATCACATGAGCATGAAGATAAAAGTCCTGAAACAGTTTTCAGTTCGGCAATTAAG
2701 TTGGAATATGCAAGGTTGGTTAAGTTGGCCCAAGAAGACACCCACCAGAAACCGATTAT
2761 CGTTTACATCATGTAGTGGTCTACTTTATCCAGAACCAGGCACCAAAGAAAATTATTGAG
2821 AAAACATTACTAGAACAATTTGGAGATAGAAATTTGAGTTTGGATGAAAGGTGTCACAAC
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2941 GAATATGAGGAGTGGCATCAGGATTATAGGAAATTCAGGGAAACAACCTATGTATCTCATA
3001 ATTGGGCTAGAAAATTTTCAAAGAGAAAGTTATATAGATTCCCTTGCTGTTTCTCATCTGT
3061 GCTTATCAGAATAACAAAGAACTCTTGTCTAAAGGCTTATACAGAGGACATGATGAAGAA
3121 TTGATATCACATTATAGAAGAGAATGTTTGCTAATCCTTAATTTAAAAAGGAAACAAAAAC
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3181 TTCGAATCTGGAGAGGATCGAGAAGTAAACAATGGTTTGATTATCATGAATGAGTTTATT
3241 GTCCCATTTTGGCATTATTACTGGTGATGAAATGGAAGAAAAGGATATACTAGCTGTA
3301 GAAGATATGAAATCGATGGTTCTTCTACCTTGGTCAAGAAATGGAACCAACCTCCAA
3361 GAAAAGCTGACAGATTTTTTGCCAAAACCTGCTTGATTGTTCTATGGAGATTAAAAGTTTC

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3421 CATGAGCCACCGAAGTTACCTTCATATTCCACGCATGAACTCTGTGAGCGATTTGCCCCGA
3481 ATCATGTTGTCCCTCAGTCGAACTCCTGCTGATGGAAGATAACTGCACACTTTCCCTGA
3541 ACACACTGTATAAACTCTTTTTAGTTCTTAACCCTTGCCTTCCTGTCACAGGGTTTGCTT
3601 GTTGCTGCTATAGTTTTTAACTTTTTTTATTTTAATAACTGCAAAAGACAAAATGACTA
3661 TACAGACTTTAGTCAGACTGCAGACAATAAAGCTGAAAATCGCATGGCGCTCAGACATT
3721 TAACCGGAAGTATGTATAATCACAAATCTAATTGATTTTATTATGGCAAACTATGCTT
3781 TTGCCACCTTCCTGTTGCAGTATTACTTTGCTTTTATCTTTTCTTCTCAACAGCTTTCC
3841 ATTCAGTCTGGATCCTTCCATGACTACAGCCATTTAAGTGTTTCAGCACTGTGTACGATAC
3901 ATAATATTTGGTAGCTTGTAATGAAATAAAGAATAAAGTTTTATTATGGCTAC

FIGURE 3B

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FIGURE 4

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1  MTVEQNVLQQSAAQKHQQTFLNQLREITGINDTQILQQALKDSNGNLELAVAFLTAKNAK
61  TPQQEETTYQTALPGNDRIYISVGSQADTNVIDLTGDDKDDLQRTIALSLAESNRAFRET
121 GITDEEQAISRVLEASIAENKACLKRTPTTEVWRDSRNPYDRKRQDKAPVGLKNVGNTCWF
181 SAVIQSLFNLLEFRRLVLNYPKPSNAQDLPRNQKEHRNLPMRELRYLFALLVGTGRKYV
241 DPSRAVEILKDAFKSNDSSQQQDVSEFTHKLLDWLEDAFQMKAEETDEEKPKNPMVELFY
301 GRFLAVGVLEGKKFENTEMFGQYPLQVNGFKDLHECLEAAMIEGEIESLHSENSGKSGQE
361 HWFTGLPPVLTFXLSRFEFNQALGRPEKIHNLKLEFPQVLYLDHYMHRNREITRIKREEIK
421 RLKDYLTVLQQRLERYLSYSGSGPKRFPLVDVLQYALEFASSKPVCTSPVDDIDASSPPSG
481 SIPSQTLPTSTTEQQGALSSSELPSTSPSSVAAISSRSVIHKPFTQSRIPDLPMHPAPRHI
541 TEEELSVLESCLHRWRTEIENDTRDLQESISRIHRTIELMYSKSMIQVPYRLHAVLVHE
601 GQANAGHYWAYIFDHRESRWMKYNDIAVTKSSWEELVRDSFGGYRNASAYCLMYINDKAQ
661 FLIQEEFNKETGQPLVGIETLPPDLRDFVEEDNQRFKELEEWDAQLAQKALQEKLLASQ
721 KLRESETSVTTAAAGDPEYLEQPSRSDFSKHLKEETIQIITKASHEHEDKSPETVLQSA
781 IKLEYARLVKLAQEDTPPETDYRLHHVVVYFIQNQAPKKIIEKTLLEQFGDRNLSFDERC
841 HNIMKVAQAKLEMIKPPEVNLEEEYEEWHQDYRKFRETTMYLIIGLENFQRESYIDSLFL
901 ICAYQNNKELLSKGLYRGHDEELISHYRRECLLILNLKRKQKPIFFFLLHCKKLNEQAA
961 ELFESGEDREVNNGLIIMNEFIVPFLPLLLVDEMEEKDILAVEDMRNRWC SYLGQEMEPH
1021 LQEKLTDFLPKLLDCSMEIKSFHEPPKLPSYSTHELCELFARIMLSLRTPADGR

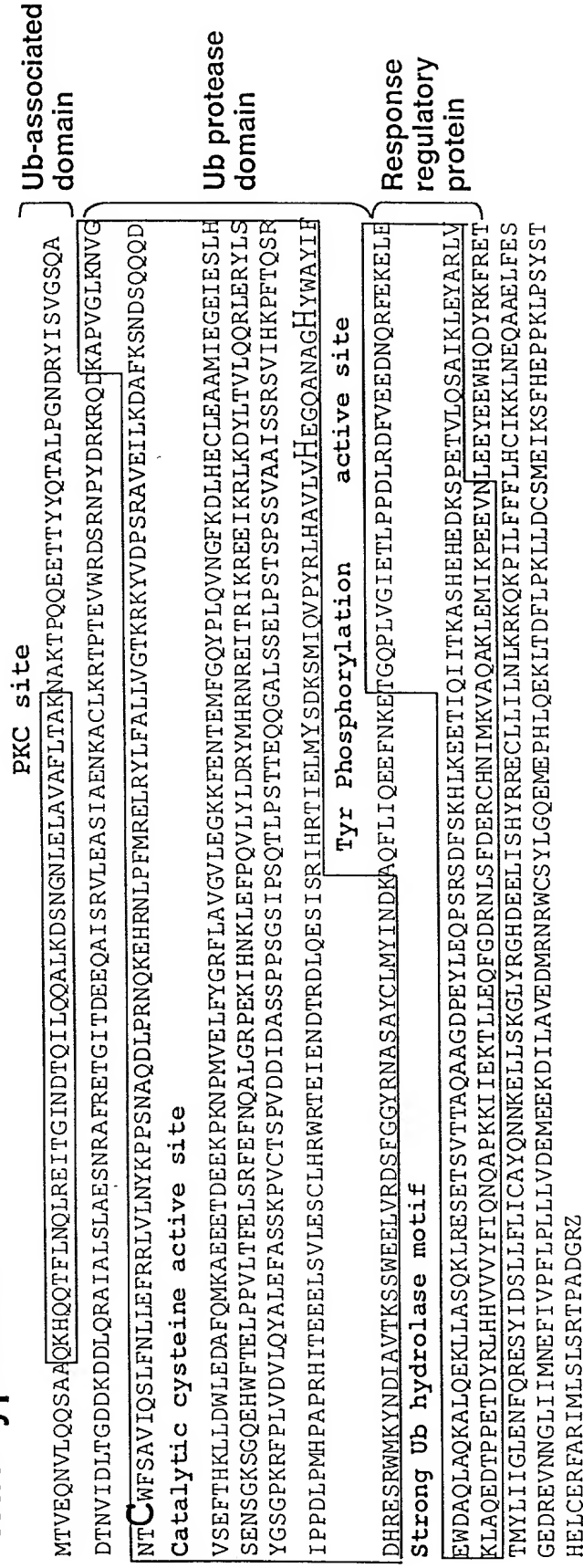
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TPQEEETTYQTALPGNDRIYISVGSQADTNVIDLTGDDKDDLQRTIALSLAESNRAFRET

Figure 5

Sequence of SUP

Wild type SUP



Mutant SUP

Cys → Ser

mtSUP Suppresses α -IgM-Induced NFAT-Luciferase Activity as a Dominant-negative Mutant

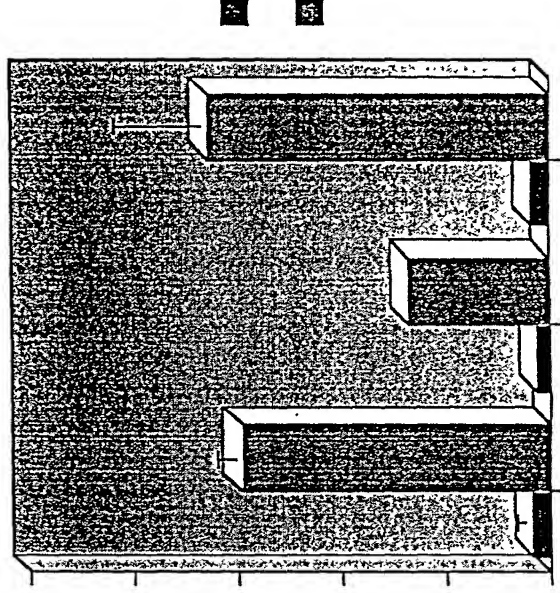
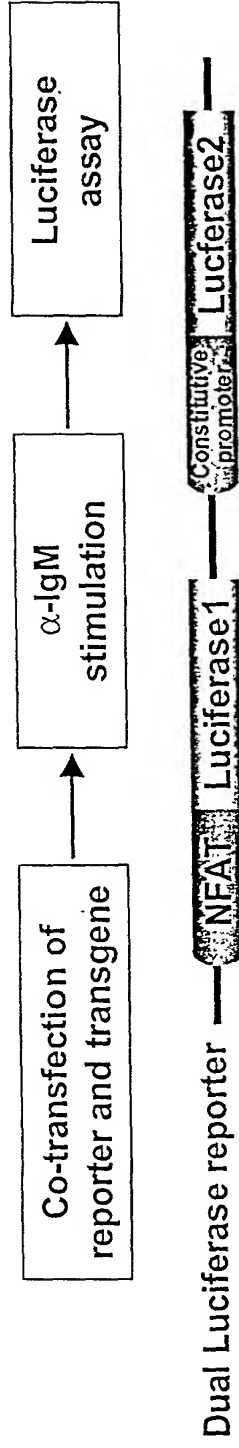
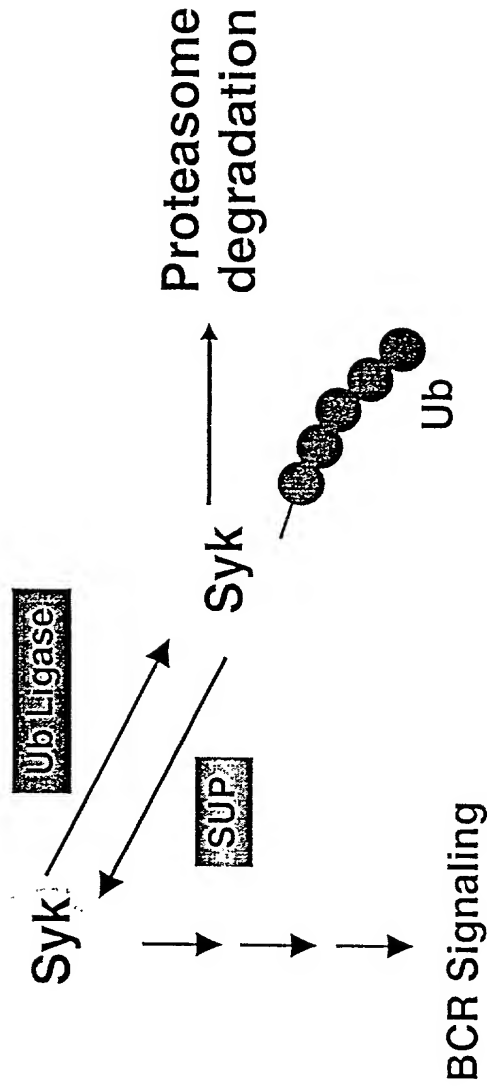


Figure 7

Model: SUP Regulates BCR Signaling by Stabilizing Syk



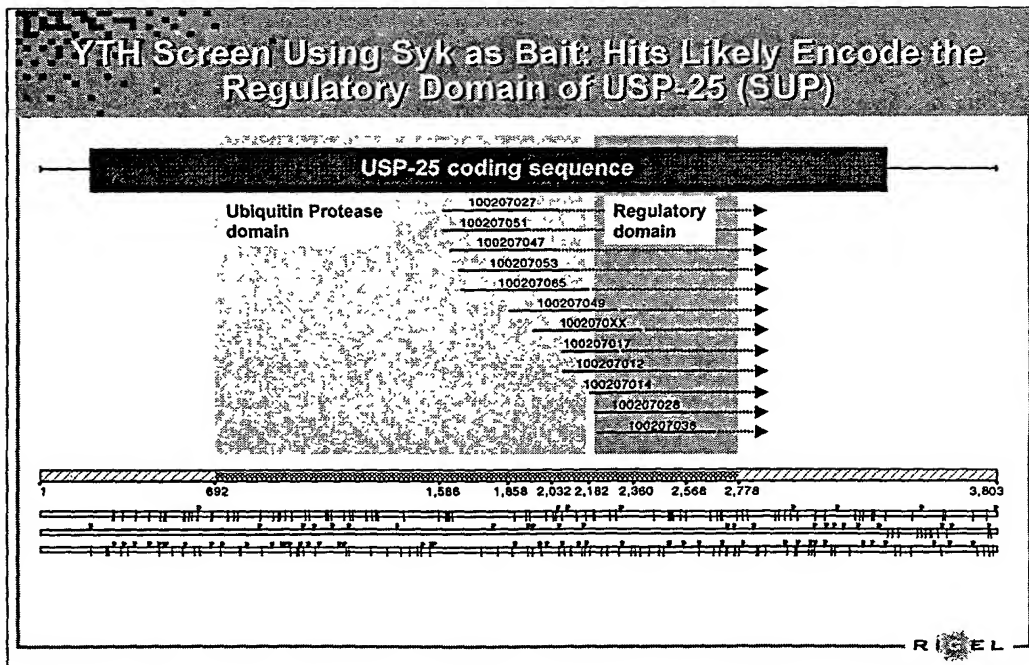


Fig. 8

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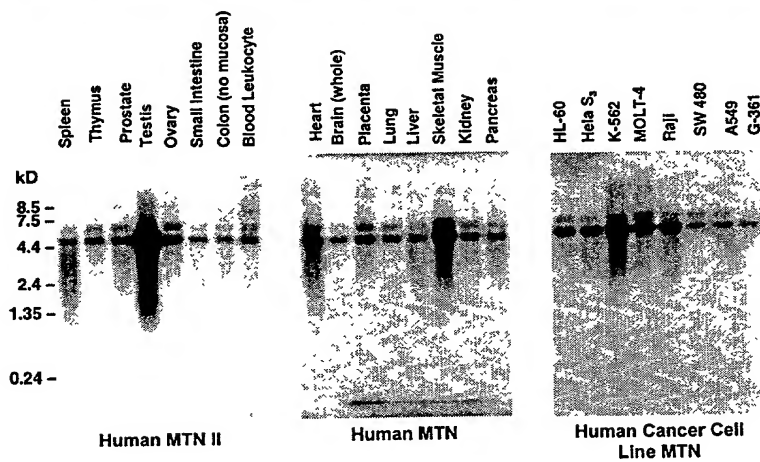
Syk Interacting Ubiquitin Protease USP-25

Wild type USP-25

MTVEQNVLQSSA **QKHQCTFFNQLREITGINDTQLOQALKDSNGNLELAVALPTAN** NAKTPQQEETTYVQTALPGNDRIYSVGSQA
DTNVIDLTGDDKDDLQRAIALSLAESNRAFRETGITDEEOAISRVLEASIAENKACLKRTPTTEVWRDSRNPYDRKRQDKAFVGLKNVGNTCW
PSAVIQSLFNLLFEPRRLVLNYPSPNAQDLPRNQKEHRNLPFMRRLRYLFALLVGTGRKYVDPSRAVEILKDAFKSNDSSQQQD
Catalytic cysteine active site
VSEFTHKLLDWLEDAFQMKABBEDEEKFKNPMVELFYGRFLAVGVLEGKKFENTEMFGQYPLQVNGPKDLHECLEAMIEGIESLHSENS
GKSGQEHWFTELPVLTFFELSRFEFQALGRPEKIHNKLEFPQVLYLDYMRNRREITRIKREIKRLKDYLTVLQRLERYLSYSGGPKRF
PLVDVLQYALEFASSKPVCTSPVDDIDASSPPSGSIPSQTLPTSTEQQALSSSELPSTSPSSVAISSRSVIHKPFTQSRIPDLPMPHAPR
HITEELSVLSECLHRWTEIENDTRDLQESISRIHRTIELMYSDEMIQVFPYRLHAVLVHegQANAGHyWAYIF
Tyr Phosphorylation Active Site Histidine
DHRSRMKYNDIAVTKSSWEELVDSFGGYENASAYCLMYINDKACFLIQEEFNKETGQPLVGIEITLPPDLRDFVEEDNQRFKEKE
Strong Ub hydrolase motif
EWDALQAKALQEKALASQKRESESVTTAQAAGDPEYLEQPSRSDFSKHLKEETIQIITKASHEHEDKSPETVLQSAIKLEYARLVKLAQ
EDTPPETDYRLHHVVVYFIQNAQPKIIIEKTLLEQFGDRNLSFDERCHNIMKVAQAKLEMIPKEEYNEEYEEWHQDYRKFRETIMYLIIGL
ENFQRESYIDSLFLICAYONNKELLKGLYRGHDEELISHYRRECLLILNLKRKQKILFFFLHCICKLNEQAELFESGEDREVNGLI
MNEFIVFPFLPLLVDMEEDKILAVEDMRNRWCSYLGQEMEPHLQEKLTDFLPKLLDCSMEIKSFHEPPLKFSYSTHELCEFRFARIMLSLSR
TPADGRZ

RIGEL

USP-25 mRNA Expression Profile



RIGEL

Fig. 9

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"1926001"

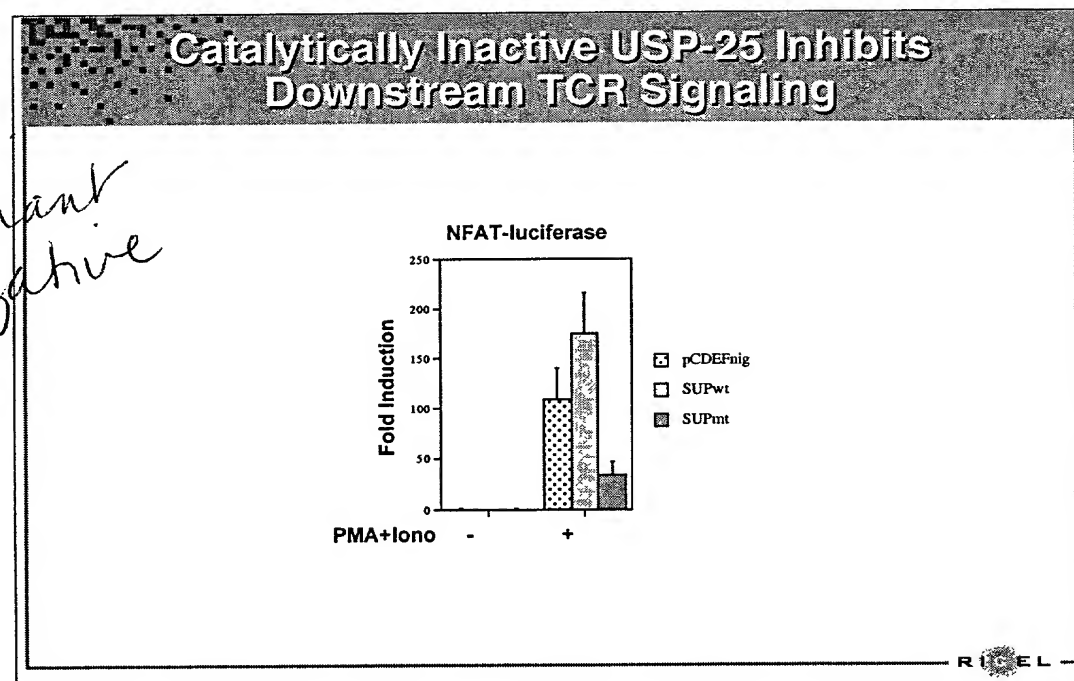
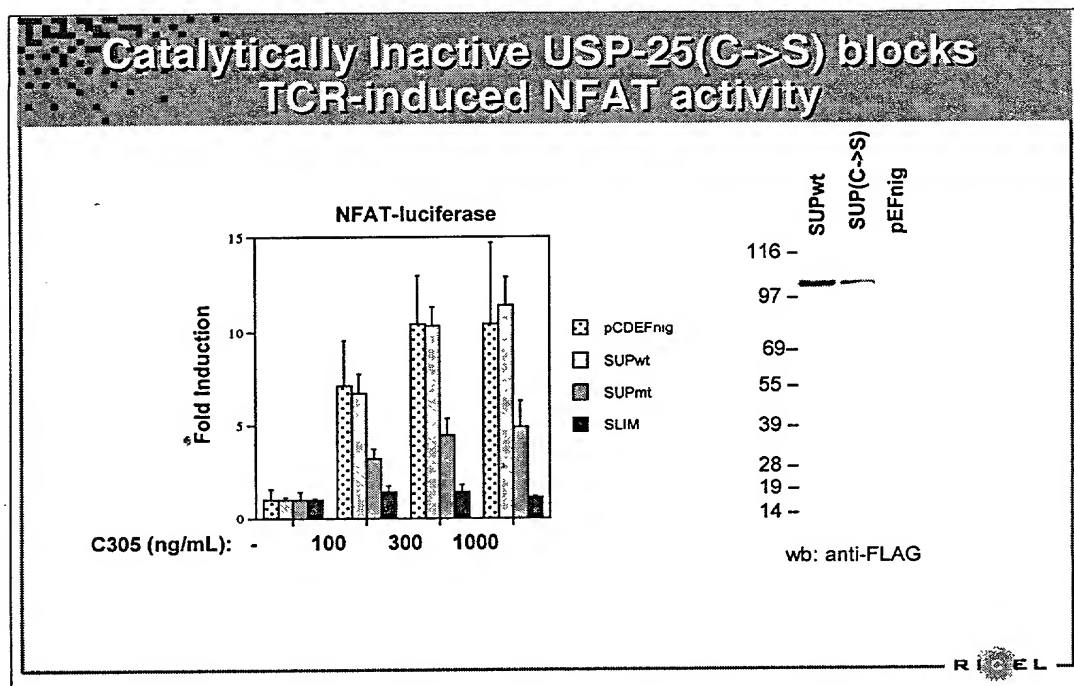


Fig. 10

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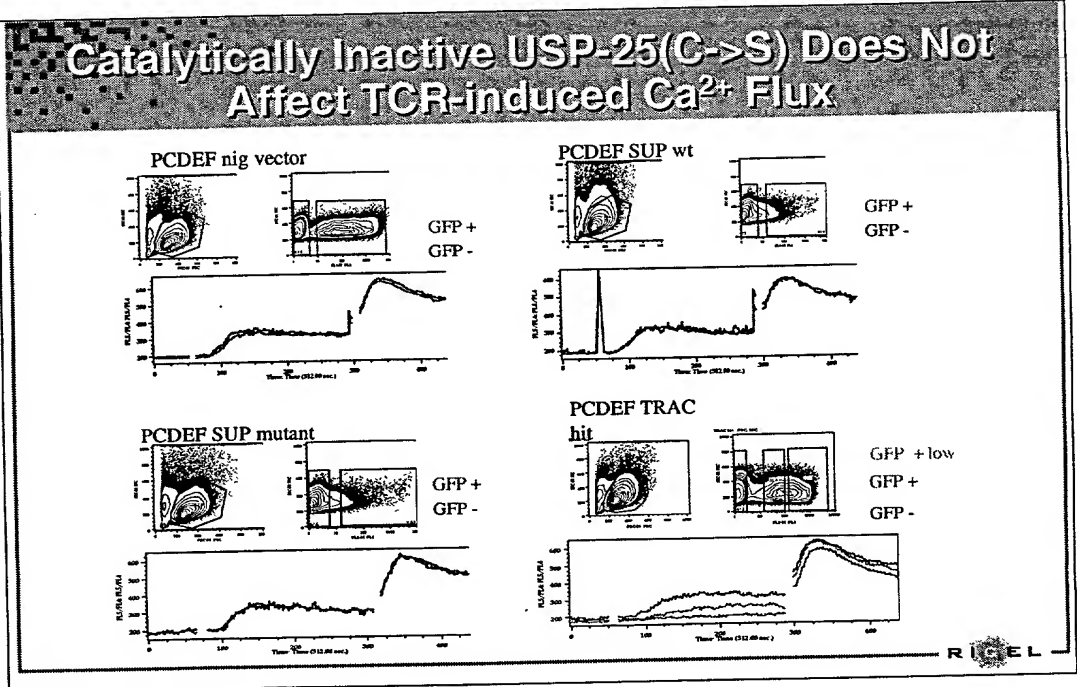
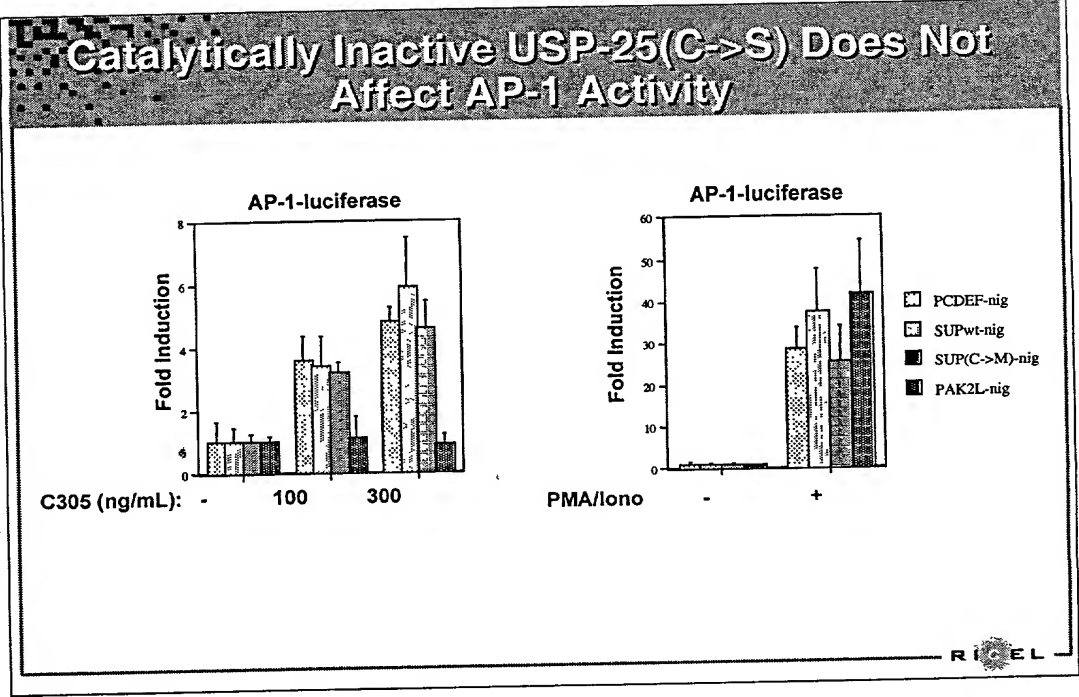


Fig. 11

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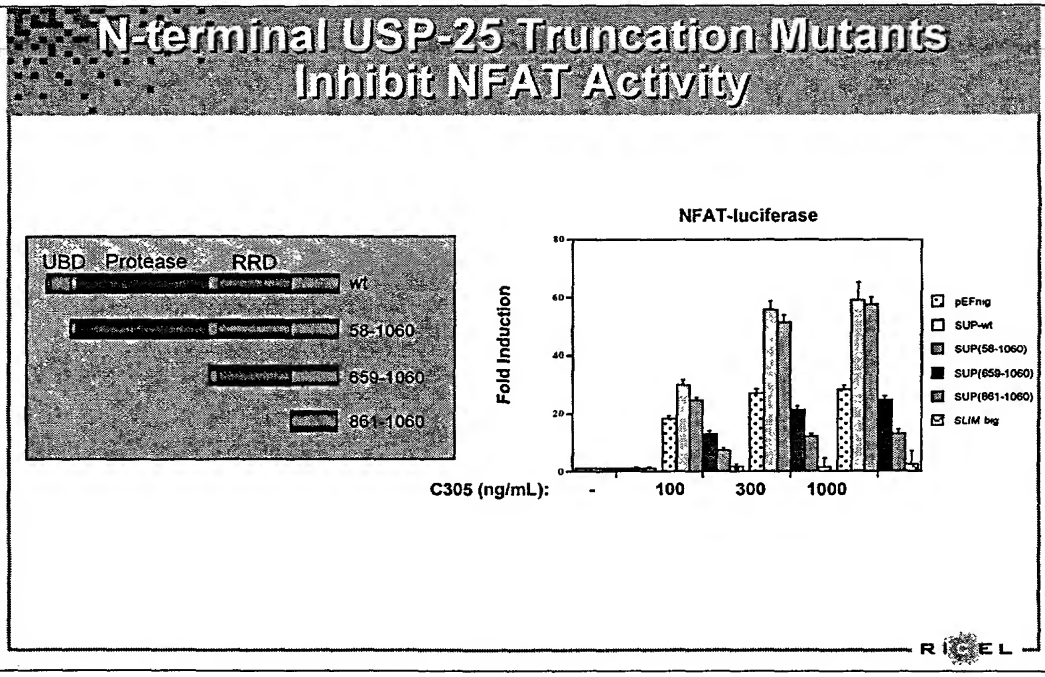
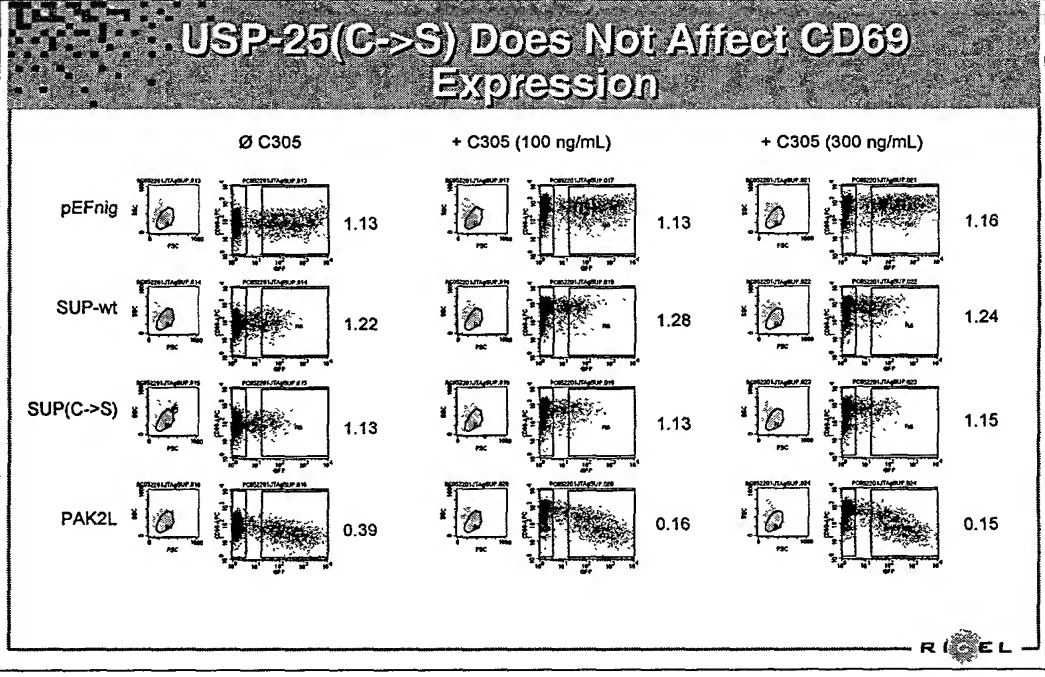


Fig. 12

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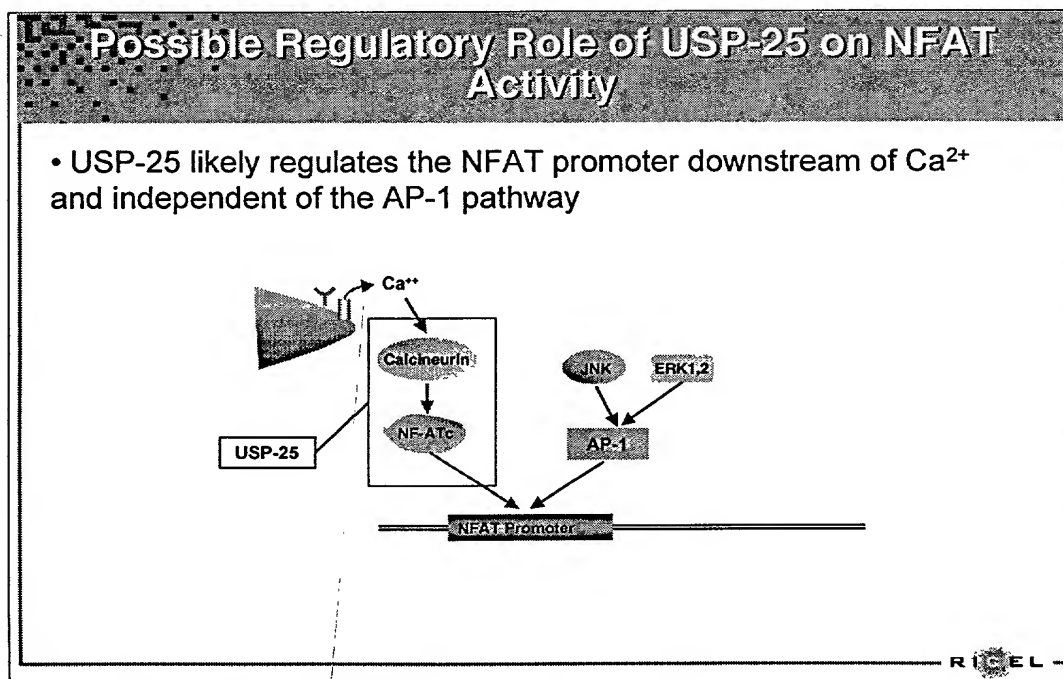
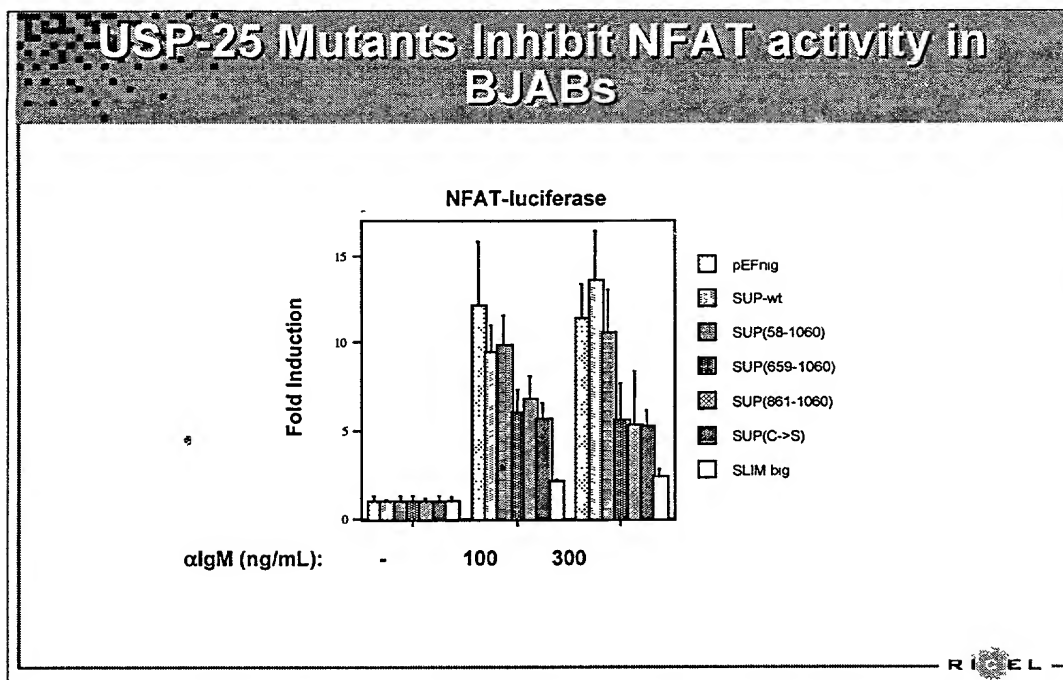


Fig. 13

Fig. 14